

GENE PRECURSOR-SEQUENCE P-SEQID GENE-SEQ G-SEQID FOLDED PRECURSOR

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GAM15 CAATGAGTCCGAGATCTTCA 1 TGAGTCCGAG 16 GA GAG-- AGA T
GACCTGGAGGAGGAGATATG ATCTTCAGAC CAAT GTCC ATCTTC CC G
AGGGACAATTG CTGG |||| ||| ||||| ||
GTTA CAGG TAGAGG GG G
A- GAGTA A-- A

GAM16 CATATGTATGTTTCAGGGAA 2 TTTTATAGAC 17 - T CAGGG GG
AGCTAGGGGATGGTTTTATA ATCACTATG CATA TG ATGTTT AAAGCTA G
GACATCACTATG |||| || ||||| |||||
GTAT AC TACAGA TTTTGGT /
C - TA--- AG

GAM17 CCACTCTATTTTGTGCATCA 3 TATGATACAG 18 CTC T ----- G T
GATGCTAAAGCATATGATAC AGGTACATAA CCA TATT TGTGC ATCA ATGC A
AGAGGTACATAATGTTTGG TGTT ||| |||| ||||| |||||
GGT GTAA ACATG TAGT TACG A
TT- T GAGACA A A

GAM18 CCATAATGATGCAGAGAGGC 4 TTAAGTGTTT 19 - T GAGA AGGAA
AATTTTAGGAACCAAAGAAA CAATTGTGG CCATAAT GA GCA GGCAATTTT C
GATTGTAAAGTGTTTCAATT ||||| || ||| |||||
GTGG GGTGTTA CT TGT TTGTTAGAA C
A T GAA- AGAAA

GAM19 CCATTGACAGAAGAAAAAAT 5 TGACAGAAGA 20 --- - AGAAAAAA AA
AAAAGCATTAGTAGAAATTT AAAAATAAAA CCAT TG ACAGA TAA G
GTACAGAGATGG GCAT |||| || ||||| |||
GGTA AC TGTTT ATT /
GAG A AAAGATG- AC

GAM20 CCTCTATTGTGTGCATCAAA 6 TATTGTGTGC 21 G ----- A AAA ATAGAGA
GGATAGAGATAAAAGACACC ATCAAAGGAT CCTCTATT TGT GC TC GG T
AAGGAAGCTTTAGACAAGAT AGAG ||||| ||| || || ||
AGAGG GGAGATAG ACA CG AG CC A
A GATTT A GAA ACAGAAA

GAM21 GAATAGTTTTTGCTGTACTT 7 TAGTTTTTGC 22 G GTACT AG
TCTATAGTGAATAGAGTTAG TGTACTTTCT GAATA TTTTGTCT TTCTAT T
GCAGGGATATTC ATAG |||| ||||| |||||
CTTAT AGGGACGG GAGATA /
- ATT-- AG

GAM22 GCCACATACCTAGAAGAATA 8 TAAGATGGGT 23 A--- GAAGAATA A - G
 AGACAGGGCTTGAAAGGAT GGCAAGTGGT GCCAC TACCTA AG CAGGG CTT G
 TTTGCTATAAGATGGGTGGC ||||| ||||| || ||||| |||
 AAGTGGT TGGTG GTGGGT TC GTTTT GGA A
 AACG AGAATA-- - A A

GAM23 GGAGACAGCGACGAAGAGCT 9 CAGACTCATC 24 C GAC A - C CAG
 CATCAGAACAGTCAGACTCA AAGCTTCTCT GGAGA AGC GA GAG CT AT A
 TCAAGCTTCTCT ||||| ||| || ||| ||| ||
 TCTCT TCG CT CTC GA TG /
 - AA- A A C ACA

GAM24 GGTCCAAAATGCGAACCCAG 10 TCCAAAATGC 25 AA GAACCC T TA
 ATTGTAAGACTATTTTAAAA GAACCCAGAT GGTCC AATGC AGAT G A
 GCATTGGGACC TGTA ||||| ||||| |||||
 CCAGG TTACG TTTA C /
 G- AAAAT- T AG

GAM25 GTA CTGGGTCTCTCTGGTTA 11 TCTCTGGTTA 26 C C A TCT CT
 GACCAGATCTGAGCCTGGGA GACCAGATCT GTA TGGGT TCTCTGGTTAG CCAGA GAGC G
 GCTCTCTGGCTAACTAGGGA GAGC || ||||| ||||| ||||| ||||| |||||
 ACCCACTGC CGT ACCCA AGGGATCAATC GGTCT CTCG G
 C - - --- AG

GAM26 TAATTGGAAGAAATCTGTTG 12 TTGGTTGCAC 27 T ----- TT
 ACTCAGATTGGTTGCACTTT TTAAATTTT TAAT GGAAGA AATCTG G
 AAATTTTCCCATTA CCCA ||||| ||||| |||||
 ATTA CCTTTT TTAGAC A
 C AAATTTACGTTGG TC

GAM27 TCTTTGGCAACGACCCCTCG 13 TGGCAACGAC 28 CAACGA CG ACA
 TCACAATAAAGATAGGGGGG CCCTCGTCAC TCTTTGG CCCCT TC A
 CAACTAAAGG AATA ||||| ||||| ||
 GGAAATC GGGGG AG T
 AACG-- AT AAA

GAM28 TTACCCTATAGTGCAGAACA 14 TATAGTGCAG 29 TATA GAACA--- C GGCAA ACA
 TCCAGGGGGCAAATGGTACAT AACATCCAGG TTACCC GTGCA TC AGG ATGGT T
 CAGGCCATATCACCTAGAAC GGCA ||||| ||||| || ||||| |||||
 TTAAATGCATGGGTAA AATGGG TACGT AG TCC TACCG /
 ---- AAATTTCA A ACTA- GAC

GAM29 TTCATTGCCAAGTTTGTTC 15 AGCCTTAGGC 30 A AG----- T
ATAACAAAAGCCTTAGGCAT ATCTCCTATG TTC TTGCCA TTTGTT C
CTCCTATGGCAGGAA GCAG ||| ||||| |||||
AAG GACGGT AAACAA A
- ATCCTCTACGGATTCCGA T

GENE	TARGET	UTR SEQUENCE	SEQID	BINDING-SITE
GAM15	PRIM2A	3' CAGGCAGATCTCAGACTC	50	C TCAGA
		GAGTC GAGATCT CCTG		
		CTCAG CTCTAGA GGAC		
		A C____		
GAM15	RAP1B	3' CCAGGTCTGAAGAACTGTTGCC	142	A CCG A
	CA	TG GT AG TCTTCAGACCTGG		
		AC CG TC AGAAGTCTGGACC		
		C TTG A		
GAM15	RET	3' CCAGGTCTAAACAGCTGACCCA	173	A CG ATCTTC
		TG GTC AG AGACCTGG		
		AC CAG TC TCTGGACC		
		C __ GACAAA		
GAM15	RET	3' CCAGGTCTAAACAGCTGACCCA	174	A CG ATCTTC
		TG GTC AG AGACCTGG		
		AC CAG TC TCTGGACC		
		C __ GACAAA		
GAM15	RET	3' CCAGGTCTAAACAGCTGACCCA	179	A CG ATCTTC
		TG GTC AG AGACCTGG		
		AC CAG TC TCTGGACC		
		C __ GACAAA		
GAM15	RET	3' CCAGGTCTAAACAGCTGACCCA	37	A CG ATCTTC
		TG GTC AG AGACCTGG		
		AC CAG TC TCTGGACC		
		C __ GACAAA		
GAM15	AMOTL1	3' CTGATAAAGATTTCAGACTCA	304	C ____
		TGAGTC GAGATCT TCAG		
		ACTCAG CTTTAGA AGTC		
		A AAT		
GAM15	DGKZ	3' CCAGACCTAGGGCTGGACTCA	70	G A C AC
		TGAGTCC AG TCTT AG CTGG		
		ACTCAGG TC GGGA TC GACC		
		_ _ _ CA		
GAM15	DKFZP586G1122	3' CAGGTCTAGCCGGGCCCA	265	A AGAT TC
		TG GTCCG CT AGACCTG		
		AC CGGGC GA TCTGGAC		
		C C____		
GAM15	FLJ22127	3' CCAGGCCTGAATGGATGGACTC	192	GAG ____ A
	A	TGAGTCC ATCT TCAG CCTGG		

			ACTCAGG TAGG AGTC GGACC	
			___ TA C	
GAM15	LOC126248	3'	CAGCCCTGGCTGGACTC 308	G ATCT AC _
			GAGTCC AG TCAG CT G	
			CTCAGG TC GGTC GA C	
			_ ____ CC A	
GAM15	LOC146640	5'	CCAGGTGACCTACCCGGACTCA 323	AGATCT AG
			TGAGTCCG TC ACCTGG	
			ACTCAGGC AG TGGACC	
			CCATCC _	
GAM15	LOC153416	3'	CCAGGTCTGAAGAACTGTTGCC 263	A CCG A
	CA		TG GT AG TCTTCAGACCTGG	
			AC CG TC AGAAGTCTGGACC	
			C TTG A	
GAM15	LOC220790	3'	CCAGGTCTGAAGAACTGTTGCC 378	A CCG A
	CA		TG GT AG TCTTCAGACCTGG	
			AC CG TC AGAAGTCTGGACC	
			C TTG A	
GAM16	PRKG2	3'	CATGGTGGTATCTTAAAA 103	T C
			TTTTA AGA ATCACTATG	
			AAAAT TCT TGGTGGTAC	
			_ A	
GAM16	AFAP	3'	CATAGCAGGGCGTCTGTAAAA 183	A_ A_
			TTTTATAGAC TC CTATG	
			AAAATGTCTG GG GATAC	
			CG AC	
GAM16	C3AR1	3'	CATAGTGAAAGTTTATAAGA 76	A_
			TTTTATAGAC TCACTATG	
			AGAATATTTG AGTGATAC	
			AA	
GAM16	FLJ22029	3'	CATGAAAATGTCTATAGAA 203	CAC
			TTTTATAGACAT TATG	
			AAGATATCTGTA GTAC	
			AAA	
GAM16	SEMA5A	3'	CATAGTGACGTCCTGAAGA 72	ATA A
			TTTT GAC TCACTATG	
			AGAA CTG AGTGATAC	
			GTC C	
GAM16	UNC5D	3'	CATAGGATTTCTATAGAA 234	C A
			TTTTATAGA ATC CTATG	

			AAGATATCT TAG GATAC		
			T _		
GAM16	LOC129446	3'	CATAGAATGTGTCTATAAA 315	CA_	
			TTTATAGACAT CTATG		
			AAATATCTGTG GATAC		
			TAA		
GAM16	LOC153396	3'	CATAGTGGCTGCCTATAGAA 338	A _	
			TTTTATAG CA TCACTATG		
			AAGATATC GT GGTGATAC		
			C C		
GAM16	LOC50999	3'	CATAATGGTGTCTTAAAA 145	T C	
			TTTTA AGACATCA TATG		
			AAAAT TCTGTGGT ATAC		
			_ A		
GAM17	KIAA0830	3'	AACATTATGCTTACTGCATC 290	A _ TA	
			GAT CAG AGG CATAATGTT		
			CTA GTC TTC GTATTACAA		
			C A _		
GAM17	PREI3	3'	AACATTATGTACTGTATATATC 275	CAGA_	
	AT		ATGATA GGTACATAATGTT		
			TACTAT TCATGTATTACAA		
			ATATG		
GAM17	SEC15L	3'	ACATATGCCTCTACTCATA 297	TAC CATA	
			TATGA AGAGGTA ATGT		
			ATACT TCTCCGT TACA		
			CA_ A__		
GAM17	LOC152317	3'	AACATCAATGGACTCTGTATCA 352	GTA A_	
			TGATACAGAG CAT ATGTT		
			ACTATGTCTC GTA TACAA		
			AG_ AC		
GAM18	DSCR1	3'	CATTTTGAAATACTTAA 81	TT	
			TTAAGTGTTCAT GTG		
			AATTCATAAAGTT TAC		
			T_		
GAM18	ELMO2	3'	CCAGGAGAAACACTTA 235	AA G	
			TAAGTGTTTC TT TGG		
			ATTCACAAAG AG ACC		
			_ G		
GAM18	ELMO2	3'	CCAGGAGAAACACTTA 186	AA G	
			TAAGTGTTTC TT TGG		

			ATTCACAAAG AG ACC	
			___ G	
GAM18	FGF5	3'	CCACAGGGAGCAAACACTTAG 227	CAA__
			TTAAGTGTTC TTGTGG	
			GATTCACAAA GACACC	
			CGAGG	
GAM18	FGF5	3'	CCACAGGGAGCAAACACTTAG 83	CAA__
			TTAAGTGTTC TTGTGG	
			GATTCACAAA GACACC	
			CGAGG	
GAM18	NEFH	3'	CCACACGTAAACACTTGA 180	CAAT
			TTAAGTGTTC TGTGG	
			AGTTCACAAA ACACC	
			TGC_	
GAM18	NFIB	3'	CCACAAAAGAAACACTTAA 93	AA
			TTAAGTGTTC TTGTGG	
			AATTCACAAAG AACACC	
			AA	
GAM18	PRKY	3'	CCATAAATGAAACACTTGA 62	A
			TTAAGTGTTC TTGTGG	
			AGTTCACAAAGT AATACC	
			A	
GAM18	RNF18	5'	CCACAATTGGGTTCTTA 172	TGT
			TAAG TTCAATTGTGG	
			ATTC GGGTTAACACC	
			TT_	
GAM18	SLC1A3	3'	CCACAATTGAAATTTTAA 77	T
			TTAAG GTTCAATTGTGG	
			AATTT TAAAGTTAACACC	
			T	
GAM18	VMD2	3'	CCATTGGAAACATTTAA 78	AATT
			TTAAGTGTTC GTGG	
			AATTTACAAAG TACC	
			GT_	
GAM18	XRCC3	5'	CCAGGGAGACACTTAA 91	AAT G
			TTAAGTGTTC T TGG	
			AATTCACAGAG G ACC	
			___ G	
GAM18	ARHGAP5	3'	CTATATGAAACATTTAA 321	AT
			TTAAGTGTTC TGTGG	

AATTTACAAAGT ATATC

GAM18	EFA6R	3'	CCATTGTGAAACACTTAA	140	ATT
			TTAAGTGTTC	GTGG	
			AATTCACAAAGT	TACC	
			GT_		
GAM18	KIAA0903	3'	CCACATGTAACACTTA	294	T AT
			TAAGTGTT CA	TGTGG	
			ATTCACAA GT	ACACC	
			T _		
GAM18	KIAA1244	3'	CCACAATTGTCTGAACAT	295	_
			GTGTTT CAATTGTGG		
			TACAAG GTTAACACC		
			TCT		
GAM18	Rpo1-2	3'	CTGTGGTAAGAACACTTAA	214	CA TG
			TTAAGTGTTC	AT TGG	
			AATTCACAAG TG	GTC	
			AA GT		
GAM18	LOC115574	3'	CCACAACCTGGAAACACTTGA	303	AA_
			TTAAGTGTTC	TTGTGG	
			AGTTCACAAAG AACACC		
			GTC		
GAM18	LOC144144	5'	CCACAATTGGGTTCTTA	260	TGT
			TAAG TTCAATTGTGG		
			ATTC GGGTTAACACC		
			TT_		
GAM18	LOC148254	3'	CCATCAAAAGAAACACTTAA	329	AA _
			TTAAGTGTTC	TTG TGG	
			AATTCACAAAG AAC ACC		
			AA T		
GAM18	LOC157624	5'	CCACTGAAACATTTAA	359	ATT
			TTAAGTGTTC	GTGG	
			AATTTACAAAGT	CACC	
			_		
GAM18	LOC220486	5'	CCACAATTGGGTTCTTA	374	TGT
			TAAG TTCAATTGTGG		
			ATTC GGGTTAACACC		
			TT_		
GAM19	AGL	3'	ATGCTTTCATTTTTC	ACTG 31	AA A
			CAG GAAAAAAT	AAAGCAT	

			GTC CTTTTTTA TTTCGTA		
			A_ C		
GAM19	AGL	3'	ATGCTTTCATTTTTTCACTG 43	AA	A
			CAG GAAAAAAT AAAGCAT		
			GTC CTTTTTTA TTTCGTA		
			A_ C		
GAM19	AGL	3'	ATGCTTTCATTTTTTCACTG 44	AA	A
			CAG GAAAAAAT AAAGCAT		
			GTC CTTTTTTA TTTCGTA		
			A_ C		
GAM19	AGL	3'	ATGCTTTCATTTTTTCACTG 45	AA	A
			CAG GAAAAAAT AAAGCAT		
			GTC CTTTTTTA TTTCGTA		
			A_ C		
GAM19	AGL	3'	ATGCTTTCATTTTTTCACTG 46	AA	A
			CAG GAAAAAAT AAAGCAT		
			GTC CTTTTTTA TTTCGTA		
			A_ C		
GAM19	AGL	3'	ATGCTTTCATTTTTTCACTG 47	AA	A
			CAG GAAAAAAT AAAGCAT		
			GTC CTTTTTTA TTTCGTA		
			A_ C		
GAM19	ALB	5'	GCTTTTCTCTTCTGTCA 40	AAAAAT	
			TGACAGAAGA AAAAGC		
			ACTGTCTTCT TTTTCG		
			C_____		
GAM19	CKN1	3'	TTTTATTCTTTCTTCTTCA 32	C	A
			TGA AGAAGAAA AATAAAA		
			ACT TCTTCTT TTATTTT		
			- C		
GAM19	HHIP	3'	TTTATTTTTTATCCTGTCA 189	AAG	
			TGACAG AAAAAATAAA		
			ACTGTC TTTTTATTT		
			CTA		
GAM19	IFNA1	3'	GCTTTCATGAATTCTGTCA 194	GAAAAA	A
			TGACAGAA AT AAAGC		
			ACTGTCTT TA TTTTCG		
			AAG__ C		
GAM19	KCNJ6	5'	TTTTTTTTTTCTTCTGCCA 60	A	T
			TG CAGAAGAAAAAA AAAA		

AC GTCTTCTTTTTT TTTT
 C T
 GAM19 OTP 3' GCTTTTATTTTATTTTATC 212 C GA
 GA AGAA AAAAATAAAAAGC
 || ||| |||||
 CT TTTT TTTTATTTTCG
 A A_

GAM19 RHEB2 3' ATGCTTCTTTTTTCTTCTGTTA 94 TAA
 TGACAGAAGAAAAA AAGCAT
 ||||| |||||
 ATTGTCTTCTTTTTT TTCGTA
 C_

GAM19 ANKRD6 3' ATGCTTTTATTCCCTTTGTTA 137 AGAAAA
 TGACAGA AATAAAAGCAT
 ||||| |||||
 ATTGTTT TTATTTTCGTA
 CCC_

GAM19 EVI5 3' TGCAGGTTTTTCTTCTTCA 95 C ATAAAA
 TGA AGAAGAAAAA GCA
 || ||||| |||
 ACT TCTTCTTTTT CGT
 _ GGA_

GAM19 FLJ00026 3' ATGCTTTGCTTTTTTCTTATG 270 G TA_
 TCA TGACA AAGAAAAA AAAGCAT
 |||| ||||| |||||
 ACTGT TTCTTTTTT TTTCGTA
 A TCG

GAM19 GP5 3' ATGCTCATATCATTTTTCTTCT 84 C _ AA
 TCA TGA AGAAGAAAAA ATA AGCAT
 || ||||| || |||||
 ACT TCTTCTTTTT TAT TCGTA
 _ AC AC

GAM19 KHDRBS3 3' ATGCTAGTTTTTTTTTCTCTT 107 C AAA
 GA AGAAGAAAAAAT AGCAT
 || ||||| |||||
 TT TCTTTTTTTTTG TCGTA
 C A_

GAM19 KIAA0254 3' TGCTGTGTTCTTTCTGTCA 132 _ AAAATAAA
 TGACAGAA GAA AGCA
 ||||| || |||||
 ACTGTCTT CTT TCGT
 T GTG_

GAM19 KIAA1165 3' ATGCTTTATAACCTCTTCTGT 281 AAAAATA
 ACAGAAGA AAAGCAT
 ||||| |||||
 TGTCTTCT TTTCGTA
 CCAATA_

GAM19 KIAA1240 3' GTGGCCATTTTTTCTTCTGTCA 277 AAAA
 TGACAGAAGAAAAAAT GC
 ||||| ||||| ||

			ACTGTCTTCTTTT	TG	
			CCGG		
GAM19	NYD-SP15	3'	ATGCCATTTTTTTCTTCTGT	209	TAAAA
			ACAGAAGAAAAA	GCAT	
			TGTCTTCTTTTT	CGTA	
			TTAC_		
GAM19	PELI1	5'	GCTTTACTCTTCTTCTGTC	175	AAATA
			GACAGAAGAAA	AAAGC	
			CTGTCTTCTTT	TTTCG	
			CTCA_		
GAM19	PRO0159	5'	TTATTTTTTCCTTGTC	125	AA
			TGACAG	GAAAAAATAA	
			ACTGTT	CTTTTTTATT	
			C_		
GAM19	RACGAP1	3'	ATGTGAGCTTTTCTTCTGTTA	121	ATAAAA
			TGACAGAAGAAAAA	GCAT	
			ATTGTCTTCTTTTT	TGTA	
			CGAG__		
GAM19	SDFR1	3'	TTATCTTTTCTTCTGTTA	118	A
			TGACAGAAGAAAA	ATAA	
			ATTGTCTTCTTTT	TATT	
			C		
GAM19	SDFR1	3'	TTATCTTTTCTTCTGTTA	151	A
			TGACAGAAGAAAA	ATAA	
			ATTGTCTTCTTTT	TATT	
			C		
GAM19	SS18L1	3'	TTATTCTATCTTCTGTCA	272	AAA
			TGACAGAAGA	AATAA	
			ACTGTCTTCT	TTATT	
			ATC		
GAM19	SV2B	3'	ATGTTTACTCTCCTTCTGTCA	136	AAAAAATAA
			TGACAGAAG	AAGCAT	
			ACTGTCTTC	TTTGTA	
			CTCTCA__		
GAM19	LOC130589	3'	TGCTTTTATTTCTCCTCCTTC	244	CA A AA
	A		TGA	GA GA AAATAAAAGCA	
			ACT	CT CT TTTATTTTCGT	
			TC	C CC	
GAM19	LOC200107	3'	ATGCTTTTACTTTTCTTTT	364	A
			AGAAGAAAAA	TAAAAGCAT	

			TTTTCTTTT	ATTTTCGTA		
			C			
GAM19	LOC203340	3'	TGCTTTTATTTTCCTTC	368	AA	
			GAAG AAAATAAAAGCA			
			CTTC TTTTATTTTCGT			
			C_			
GAM19	LOC221271	3'	TGCCTTTTTTTTCTGTCA	380	ATAAAA	
			TGACAGAAGAAAAA GCA			
			ACTGTCTTTTTTTT CGT			
			C_____			
GAM19	LOC254778	3'	ATGCTTTTCTTCTATCA	400	C	AAATAAA
			TGA AGAAGAAA AGCAT			
			ACT TCTTCTTT TCGTA			
			A _____			
GAM19	LOC51312	5'	GCTTTTATTTTCTCCTCT	164	A A	
			AGA GA AAAATAAAAGC			
			TCT CT TTTTATTTTCG			
			C C			
GAM19	LOC91286	5'	TTTTTATTTCTTTTTCTGTCA	273	A	
			TGACAGAAGAA AAATAAAAG			
			ACTGTCTTTTT TTTATTTT			
			C			
GAM19	LOC92223	3'	ATGCTTTTATTGTACCTTC	286	AAAA	
			GAAG AATAAAAGCAT			
			CTTC TTATTTTCGTA			
			CATG			
GAM19	LOC92482	5'	TGCATCTTTTCTTCTGT	288	A AAAA	
			ACAGAAGAAAA AT GCA			
			TGTCTTCTTTT TA CGT			
			C _____			
GAM20	ATRN	3'	CTATCTGATGCACAGAA	248	G	AAG
			TT TGTGCATCA GATAG			
			AA ACACGTAGT CTATC			
			G _____			
GAM20	ATRN	3'	CTATCTGATGCACAGAA	248	G	AAG
			TT TGTGCATCA GATAG			
			AA ACACGTAGT CTATC			
			G _____			
GAM20	DKFZP564O0463	3'	CTTTTCTTAATGCATACAATA	127	CAA	T
			TATTGTGTGCAT AGGA AGAG			

		ATAACATACGTA TTCT TTTC		
		A__ T		
GAM20	DKFZP564O0463 3'	CTTTTTCTTAATGCATACAATA 127	CAA	T
		TATTGTGTGCAT AGGA AGAG		
		ATAACATACGTA TTCT TTTC		
		A__ T		
GAM20	FLJ13102 3'	CTCTACCCTCTCCCACCACACA 202	CATCAA_	A
	GTA	TATTGTGTG AGG TAGAG		
		ATGACACAC TCC ATCTC		
		CACCCTC C		
GAM20	FLJ13102 3'	CTCTACCCTCTCCCACCACACA 202	CATCAA_	A
	GTA	TATTGTGTG AGG TAGAG		
		ATGACACAC TCC ATCTC		
		CACCCTC C		
GAM20	HSPC014 3'	CTGTAATTTGATGTACACAA 144	GG	
		TTGTGTGCATCAAA ATAG		
		AACACATGTAGTTT TGTC		
		AA		
GAM20	HSPC014 3'	CTGTAATTTGATGTACACAA 144	GG	
		TTGTGTGCATCAAA ATAG		
		AACACATGTAGTTT TGTC		
		AA		
GAM20	KIAA0040 3'	TCTATCCCCTTGTACATA 129	_ TCAAA	
		TGTGTG CA GGATAGA		
		ATACAC GT CCTATCT		
		T TCC__		
GAM20	KIAA0040 3'	TCTATCCCCTTGTACATA 129	_ TCAAA	
		TGTGTG CA GGATAGA		
		ATACAC GT CCTATCT		
		T TCC__		
GAM20	KIAA0470 3'	CCACTTGATGCACAAATA 134	G A_	
		TATT TGTGCATCAA GG		
		ATAA ACACGTAGTT CC		
		_ CA		
GAM20	KIAA0470 3'	CCACTTGATGCACAAATA 134	G A_	
		TATT TGTGCATCAA GG		
		ATAA ACACGTAGTT CC		
		_ CA		
GAM20	KIAA1908 5'	CTCTCGGGCGATGCACACAA 302	AAAGGAT	
		TTGTGTGCATC AGAG		

			AACACACGTAG	TCTC	
			CGGGC__		
GAM20	KIAA1908	5'	CTCTCGGGCGATGCACACAA	302	AAAGGAT
			TTGTGTGCATC	AGAG	
			AACACACGTAG	TCTC	
			CGGGC__		
GAM20	MGC22014	3'	CTCTATCCTTGTATATCACAAT	269	TGCATCA
	A		TATTGTG	AAGGATAGAG	
			ATAACAC	TTCCTATCTC	
			TATATG_		
GAM20	MGC22014	3'	CTCTATCCTTGTATATCACAAT	269	TGCATCA
	A		TATTGTG	AAGGATAGAG	
			ATAACAC	TTCCTATCTC	
			TATATG_		
GAM20	TNRC9	3'	CTGTATTTTGATGCAACAA	293	G G
			TTGT TGCATCAAAG	ATAG	
			AACA ACGTAGTTTT	TGTC	
			_	A	
GAM20	TNRC9	3'	CTGTATTTTGATGCAACAA	293	G G
			TTGT TGCATCAAAG	ATAG	
			AACA ACGTAGTTTT	TGTC	
			_	A	
GAM20	LOC116123	3'	CTTTGGTTTGATGCATACAATA	243	GGA
			TATTGTGTGCATCAA	TAGAG	
			ATAACATACGTAGTTT	GTTTC	
			G__		
GAM20	LOC116123	3'	CTTTGGTTTGATGCATACAATA	243	GGA
			TATTGTGTGCATCAA	TAGAG	
			ATAACATACGTAGTTT	GTTTC	
			G__		
GAM20	LOC149721	3'	CTATCATGTGGATGCACACA	334	AAAG_
			TGTGTGCATC	GATAG	
			ACACACGTAG	CTATC	
			GTGTA		
GAM20	LOC149721	3'	CTATCATGTGGATGCACACA	334	AAAG_
			TGTGTGCATC	GATAG	
			ACACACGTAG	CTATC	
			GTGTA		
GAM20	LOC153338	5'	CTCTATCCCTCTGTGGCCAATA	354	T G CAAA
			TATTG GT CAT	GGATAGAG	

			ATAAC CG GTG CCTATCTC		
			— — TCTC		
GAM20	LOC153338	5'	CTCTATCCCTCTGTGGCCAATA 354	T G	CAAA
			TATTG GT CAT GGATAGAG		
			ATAAC CG GTG CCTATCTC		
			— — TCTC		
GAM20	LOC220766	3'	CCACTTGATGCACAAATA 375	G	A_
			TATT TGTGCATCAA GG		
			ATAA ACACGTAGTT CC		
			— CA		
GAM20	LOC220766	3'	CCACTTGATGCACAAATA 375	G	A_
			TATT TGTGCATCAA GG		
			ATAA ACACGTAGTT CC		
			— CA		
GAM20	LOC253351	5'	CTGGCACCTGATGCACACAA 402		AAGGA
			TTGTGTGCATCA TAG		
			AACACACGTAGT GTC		
			CCACG		
GAM20	LOC253351	5'	CTGGCACCTGATGCACACAA 402		AAGGA
			TTGTGTGCATCA TAG		
			AACACACGTAGT GTC		
			CCACG		
GAM20	LOC257484	3'	CTCTATCCTTGTATATCACAAT 366		TGCATCA
	A		TATTGTG AAGGATAGAG		
			ATAACAC TTCCTATCTC		
			TATATG_		
GAM20	LOC257484	3'	CTCTATCCTTGTATATCACAAT 366		TGCATCA
	A		TATTGTG AAGGATAGAG		
			ATAACAC TTCCTATCTC		
			TATATG_		
GAM21	KIAA1843	3'	ATAGAAAGTAGCCAAAAA 267	CTG	
			TTTTTG TACTTTCTAT		
			AAAAAC ATGAAAGATA		
			CG_		
GAM21	SDFR1	3'	AAAGTACAGCAAAACCTA 117	T	
			TAG TTTTGCTGTACTTT		
			ATC AAAACGACATGAAA		
			C		
GAM21	SDFR1	3'	AAAGTACAGCAAAACCTA 150	T	
			TAG TTTTGCTGTACTTT		

			ATC AAAACGACATGAAA		
			C		
GAM21	LOC132617	3'	CTACAGACCATAGCAAAAAC 314	ACTT	A
			GTTTTTGCTGT TCT TAG		
			CAAAAACGATA AGA ATC		
			CC__ C		
GAM21	LOC145622	3'	CTATAGAACAATGCAAAAAC 322	TGTACT	
			GTTTTTGC TTCTATAG		
			CAAAAACG AAGATATC		
			TAAC__		
GAM21	LOC222681	3'	CTACAGAACATGGAGCAAAAAC 386	G CT	A
	TA		TAGTTTTTGCT TA TTCT TAG		
			ATCAAAAACGA GT AAGA ATC		
			G AC C		
GAM21	LOC257507	3'	CTACAGAACATGGAGCAAAAAC 405	G CT	A
	TA		TAGTTTTTGCT TA TTCT TAG		
			ATCAAAAACGA GT AAGA ATC		
			G AC C		
GAM21	LOC257625	3'	CTACAGAACATGGAGCAAAAAC 406	G CT	A
	TA		TAGTTTTTGCT TA TTCT TAG		
			ATCAAAAACGA GT AAGA ATC		
			G AC C		
GAM22	BTEB1	3'	ACCACTACATCCATCT 53	GCA	
			AGATGGGTG AGTGGT		
			TCTACCTAC TCACCA		
			A__		
GAM22	CEP2	3'	ACCACCTCCTTCATCTT 112	T CAA	
			AAGATGGG GG GTGGT		
			TTCTACTT CC CACCA		
			_ TC_		
GAM22	ECM1	3'	ACCCTGCCCCACCCATCT 82	CA_ T	
			AGATGGGTGG AG GGT		
			TCTACCCACC TC CCA		
			CCG _		
GAM22	ENG	3'	ACCACTTGCCACGCTGTT 34	_	
			GATGG GTGGCAAGTGGT		
			TTGTC CACCGTTCACCA		
			G		
GAM22	ESRRG	3'	ACCACTTTTCAGCCATTT 276	G C	
			AGATGG TGG AAGTGGT		

			TTTACC ACT TTCACCA		
			G T		
GAM22	HDAC4	3'	ACCACTCGACTCATCTTG 98	GGCA	
			TAAGATGGGT AGTGGT		
			GTTCTACTCA TCACCA		
			GC__		
GAM22	IL6	3'	ACCACTTGAAACATTTTA 41	GGTGG	
			TAAGATG CAAGTGGT		
			ATTTTAC GTTCACCA		
			AAA__		
GAM22	LRAT	3'	ACCACTTAAAATTATCTTA 259	GTGGC	
			TAAGATGG AAGTGGT		
			ATTCTATT TTCACCA		
			AAAA_		
GAM22	MYLK2	3'	ACCACTCGGGGCCCCCATCTTG 226	T A__	
			TAAGATGGG GGC AGTGGT		
			GTTCTACCC CCG TCACCA		
			_ GGGC		
GAM22	PRKACB	3'	ACCACTTCTTTTCATCT 61	T C	
			AGATGGG GG AAGTGGT		
			TCTACTT TC TTCACCA		
			T _		
GAM22	PRLR	3'	ACCACTTGCCTCTTTCT 51	T T	
			AGA GGG GGCAAGTGGT		
			TCT TCT CCGTTCACCA		
			T _		
GAM22	SLC6A6	3'	ACCACTTGAATTGATCTT 65	G GG	
			AAGAT GGT CAAGTGGT		
			TTCTA TTA GTTCACCA		
			G A_		
GAM22	WASF3	3'	ACCACTTGGTCAGAATTTTA 109	GGG _	
			TAAGAT TGGC AAGTGGT		
			ATTTTA ACTG TTCACCA		
			AG_ G		
GAM22	XK	3'	ACCACTTGCACTATTCTTA 181	TG G	
			TAAGA GGTG CAAGTGGT		
			ATTCT TCAC GTTCACCA		
			TA _		
GAM22	ZYX	3'	ACCACCTGCCCCCACCT 69	A T A	
			AG TGGG GGCA GTGGT		

			TC ACCC CCGT CACCA	
			C _ C	
GAM22	ARHF	3'	ACCCTGGACCACCCATCT 167	CA_ T
			AGATGGGTGG AG GGT	
			TCTACCCACC TC CCA	
			AGG _	
GAM22	DDR1	5'	CGCACCACCCATTTTA 57	CAA
			TAAGATGGGTGG GTG	
			ATTTTACCCACC CGC	
			A__	
GAM22	DDR1	5'	CGCACCACCCATTTTA 122	CAA
			TAAGATGGGTGG GTG	
			ATTTTACCCACC CGC	
			A__	
GAM22	DDR1	5'	CGCACCACCCATTTTA 123	CAA
			TAAGATGGGTGG GTG	
			ATTTTACCCACC CGC	
			A__	
GAM22	DKFZP547E1010	5'	ACCACCTCCCTATCTTA 141	TG CAA
			TAAGATGGG G GTGGT	
			ATTCTATCC C CACCA	
			CT__	
GAM22	DKFZP547E1010	5'	ACCACCTCCCTATCTTA 280	TG CAA
			TAAGATGGG G GTGGT	
			ATTCTATCC C CACCA	
			CT__	
GAM22	FLJ11715	3'	ACCGCGCCCAGCCCATCT 197	_ AA
			AGATGGGT GGC GTGGT	
			TCTACCCG CCG CGCCA	
			AC _	
GAM22	FLJ12587	3'	ACCAGGGCCGCATCCATCT 190	_ AAG
			AGATGG GTGGC TGGT	
			TCTACC CGCCG ACCA	
			TA GG_	
GAM22	FLJ12650	3'	ACCACTTGCCAATGCCTCTC 196	T _
			GA GGGT GGCAAGTGGT	
			CT TCCG CCGTTCACCA	
			C TAA	
GAM22	FLJ13265	3'	ACCACTTGCCCTGCCTCA 201	_ _
			TG GGT GGCAAGTGGT	

			AC CCG CCGTTCACCA		
			T TC		
GAM22	FLJ20546	3'	ACCTCTGCCACCCATCT 155	A T	
			AGATGGGTGGCA G GGT		
			TCTACCCACCGT C CCA		
			_ T		
GAM22	FLJ32865	3'	ACCACCACGCCCAGCTTA 251	A GCAA	
			TAAG TGGGTG GTGGT		
			ATTC ACCCGC CACCA		
			G AC__		
GAM22	GPR88	3'	ACCACTTGTTGTACATCT 185	G TG	
			AGATG G GCAAGTGGT		
			TCTAC T TGTTACCA		
			A GT		
GAM22	HSPC216	3'	ACCTGACCACCCATTT 149	_ AGT	
			AGATGGGTGG CA GGT		
			TTTACCCACC GT CCA		
			A ____		
GAM22	JKI	3'	ACCACATTCCCCATTTTA 148	T CAA	
			TAAGATGGG GG GTGGT		
			ATTTTACCC CT CACCA		
			_ TA_		
GAM22	KIAA0153	3'	ACCACCCAGCAAGCCCGCCTTA 139	A G_ AA_	
			TAAG TGGGT GC GTGGT		
			ATTC GCCCG CG CACCA		
			C AA ACC		
GAM22	KIAA0215	3'	ACCAGGAGACCACCATCTTA 130	G CAAG_	
			TAAGATGG TGG TGGT		
			ATTCTACC ACC ACCA		
			_ AGAGG		
GAM22	KIAA0461	3'	ACCACTTGTTGAAATCCA 291	_____	
			TGGGT GGCAAGTGGT		
			ACCTA TTGTTCACCA		
			AAG		
GAM22	MEGF10	3'	ACCACAGACTCATCTTA 216	GGCAA	
			TAAGATGGGT GTGGT		
			ATTCTACTCA CACCA		
			GA__		
GAM22	MGC2452	5'	ACCACTAATTGCCACTCA 218	_____	
			TGGGTGGCA AGTGGT		

			ACTCACCGT TCACCA		
			TAA		
GAM22	MGC4796	3'	ACCTTCACCTCATCTTA 266	_	CAAGT
			TAAGATG GGTGG GGT		
			ATTCTAC CCACT CCA		
			T T__		
GAM22	MRPL10	3'	ACCACATTGTACCCATT 256	G	_
			AGATGGGTG CAA GTGGT		
			TTTACCCAT GTT CACCA		
			_ A		
GAM22	MRPL42	5'	ACCACTTGATAAGCATCTTG 299	GG	G
			TAAGATG TG CAAGTGGT		
			GTTCTAC AT GTTCACCA		
			GA A		
GAM22	POLYDOM	3'	ACCACTGCTATCCATCTT 195		A
			AAGATGGGTGGCA GTGGT		
			TTCTACCTATCGT CACCA		
			-		
GAM22	PRO0246	5'	ACCACTTGCTATGGTCT 126	GG	
			AGAT GTGGCAAGTGGT		
			TCTG TATCGTTCACCA		
			G_		
GAM22	SMCR7	3'	ATGACTTGCCACCCACCT 247	A	G
			AG TGGGTGGCAAGT GT		
			TC ACCCACCGTTCA TA		
			C G		
GAM22	TPD52	3'	ACCACTTATATCAACTTA 88	ATG	GC
			TAAG GGTG AAGTGGT		
			ATTC CTAT TTCACCA		
			AA_ A_		
GAM22	ZNF384	3'	ACCACTCATCACGGCCATCTT 239	_	CA
			AAGATGG GTGG AGTGGT		
			TTCTACC CACT TCACCA		
			GG AC		
GAM22	LOC124216	3'	ACCTCTCCTCACCCATCTTA 307	CA	T
			TAAGATGGGTGG AG GGT		
			ATTCTACCCACT TC CCA		
			CC T		
GAM22	LOC144509	5'	ACCACCAGCTGCACCCATCT 320	_	AA
			AGATGGGTG GC GTGGT		

		TCTACCCAC CG CACCA		
		GT AC		
GAM22	LOC146822 3'	ACCACCTGCCCTACCATT 324	GT_	A
		AGATGG GGCA GTGGT		
		TTTACC CCGT CACCA		
		ATC C		
GAM22	LOC148371 5'	ACCACTTCTGGCCATCT 330	G	C
		AGATGG TGG AAGTGGT		
		TCTACC GTC TTCACCA		
		G _		
GAM22	LOC149373 3'	ACCTGCCGGCCACCCATTCA 333	A	AA _
		A GATGGGTGGC GT GGT		
		A TTACCCACCG CG CCA		
		C GC T		
GAM22	LOC151146 5'	ACCCCCAGCCCATCTTA 336	_	CAAGT
		TAAGATGGG TGG GGT		
		ATTCTACCC ACC CCA		
		G CC__		
GAM22	LOC157562 5'	ACCACCCAGTCATTTTA 357	G	CAA
		TAAGATGG TGG GTGGT		
		ATTTTACT ACC CACCA		
		G _		
GAM22	LOC160897 3'	ACCACTTATAATGCCTCATCTT 341	_	GC__
	A	TAAGATG GGTG AAGTGGT		
		ATTCTAC CCGT TTCACCA		
		T AATA		
GAM22	LOC161589 5'	ACCACTGCTGGCCATCT 343	G	A
		AGATGG TGGCA GTGGT		
		TCTACC GTCGT CACCA		
		G _		
GAM22	LOC163682 5'	ACCACTTGCCGAGCTCCTA 361	_____	
		TGGG TGGCAAGTGGT		
		ATCC GCCGTTCACCA		
		TCGA		
GAM22	LOC199692 3'	ACCAGTAACCTATCTTA 257	G	AAG
		TAAGATGGGT GC TGGT		
		ATTCTATCCA TG ACCA		
		A _		
GAM22	LOC202108 5'	ACCACTACTGGCCATCT 367	G	CA
		AGATGG TGG AGTGGT		

			TCTACC GTC TCACCA		
			G A_		
GAM22	LOC221468	3'	ACCACCCAGTTCTTCATCTT 258		TG AA_
			AAGATGGG GC GTGGT		
			TTCTACTT TG CACCA		
			CT ACC		
GAM22	LOC221838	5'	ACCACTACTGGCCATCT 385		G CA
			AGATGG TGG AGTGGT		
			TCTACC GTC TCACCA		
			G A_		
GAM22	LOC221839	5'	ACCACTACTGGCCATCT 384		G CA
			AGATGG TGG AGTGGT		
			TCTACC GTC TCACCA		
			G A_		
GAM22	LOC90313	5'	ACCACCCCTGTGCCCATC 268		G A__
			GATGGGTG CA GTGGT		
			CTACCCGT GT CACCA		
			_ CCC		
GAM22	LOC92399	3'	ACCACCTGCTCCTCATCTTA 242		TG A
			TAAGATGGG GCA GTGGT		
			ATTCTACTC CGT CACCA		
			CT C		
GAM23	ADAM8	3'	AGAGAAGCCATGCGTTCC 52	A T	CAA
			C GAC CAT GCTTCTCT		
			C TTG GTA CGAAGAGA		
			C C C_		
GAM23	BN51T	3'	AGAGAGCAAGGATTGAGTCTG 363	_ AA_ T	
			CAGACTCA TC GCT CTCT		
			GTCTGAGT AG CGA GAGA		
			T GAA _		
GAM23	CD3Z	3'	AGACTGACCTTGATGAGCTG 48	A	C C_
			CAG CTCATCAAG TT TCT		
			GTC GAGTAGTTC AG AGA		
			_ C TC		
GAM23	DAAM2	3'	AGGTGCTTGATGAATCTG 381	C	T
			CAGA TCATCAAGC TCT		
			GTCT AGTAGTTCG GGA		
			A T		
GAM23	DLG4	3'	AGGGAGGGATGGGTCT 54	AAG	
			AGACTCATC CTTCTCT		

TCTGGGTAG GGAGGGA

GAM23	DMD	5' AGAAAAGCTTGAGCAAGTC 73	CA_	C
		GACT TCAAGCTT TCT		
		CTGA AGTTCGAA AGA		
		ACG A		
GAM23	DMD	5' AGAAAAGCTTGAGCAAGTC 74	CA_	C
		GACT TCAAGCTT TCT		
		CTGA AGTTCGAA AGA		
		ACG A		
GAM23	DMD	5' AGAAAAGCTTGAGCAAGTC 75	CA_	C
		GACT TCAAGCTT TCT		
		CTGA AGTTCGAA AGA		
		ACG A		
GAM23	E2F1	3' AGGCCTCTTTGGTGAGCCTG 348	A	_____
		CAG CTCATCAA GCTT		
		GTC GAGTGGTT CGGA		
		C TCTC		
GAM23	EBP	3' AGAGAAGCCAGGAGGTCT 108	CA AA_	
		AGACT TC GCTTCTCT		
		TCTGG AG CGAAGAGA		
		_ GAC		
GAM23	FANCG	5' AGAGAAGCAGGGGAGCTC 85	_ A AA	
		GA CTC TC GCTTCTCT		
		CT GAG GG CGAAGAGA		
		C _ GA		
GAM23	FE65L2	5' AGGCGCCTGATGAGTTCA 99	A	A T
		C GACTCATCA GC TCT		
		A TTGAGTAGT CG GGA		
		C C C		
GAM23	FE65L2	5' AGGCGCCTGATGAGTTCA 236	A	A T
		C GACTCATCA GC TCT		
		A TTGAGTAGT CG GGA		
		C C C		
GAM23	FE65L2	5' AGGCGCCTGATGAGTTCA 237	A	A T
		C GACTCATCA GC TCT		
		A TTGAGTAGT CG GGA		
		C C C		
GAM23	FE65L2	5' AGGCGCCTGATGAGTTCA 238	A	A T
		C GACTCATCA GC TCT		

			A TTGAGTAGT CG GGA		
			C C C		
GAM23	FGFR4	3'	AGAGAAGCTGGAAGCCTG 193	A CA A	
			CAG CT TC AGCTTCTCT		
			GTC GA AG TCGAAGAGA		
			C _ G		
GAM23	FGFR4	3'	AGAGAAGCTGGAAGCCTG 58	A CA A	
			CAG CT TC AGCTTCTCT		
			GTC GA AG TCGAAGAGA		
			C _ G		
GAM23	FHL1	3'	AGAGAAGCTGATGCCTC 55	CT A	
			GA CATCA GCTTCTCT		
			CT GTAGT CGAAGAGA		
			CC _		
GAM23	GCNT2	5'	AGAGAAACGAGTGAGTTTG 56	CAAGC	
			CAGACTCAT TTCTCT		
			GTTTGAGTG AAGAGA		
			AGCA_		
GAM23	GNRHR	5'	AGAGAAGCTGGTAATTCTG 38	CTC A	
			CAGA ATCA GCTTCTCT		
			GTCT TGGT CGAAGAGA		
			TAA _		
GAM23	HIS1	5'	AGGGGAGATGAGTTTG 105	AAG	
			CAGACTCATC CTTCT		
			GTTTGAGTAG GGGGA		
			A_		
GAM23	HNRPDL	3'	AGAAAGGTATGAGTTTG 92	CAA C	
			CAGACTCAT GCTT TCT		
			GTTTGAGTA TGGA AGA		
			_ A		
GAM23	INHBA	3'	AGAAAGCCATGAGTTTG 59	CAA C	
			CAGACTCAT GCTT TCT		
			GTTTGAGTA CGAA AGA		
			C_ _		
GAM23	KIF3B	3'	AGAGAAGCTCATAAGTGTG 87	G C CA	
			CA ACT AT AGCTTCTCT		
			GT TGA TA TCGAAGAGA		
			G A C_		
GAM23	MSN	3'	AGAGAAGCCTGTGCCCTG 262	ACT T A	
			CAG CA CA GCTTCTCT		

			GTC GT GT CGAAGAGA		
			CC_ _ C		
GAM23	MTR	3'	AGAGAAGTGTGACCCTG 36	AC CAA	
			CAG TCAT GCTTCTCT		
			GTC AGTG TGAAGAGA		
			CC _		
GAM23	PCDHB9	3'	AGAGAAGTTAGATCCTG 169	ACTC A	
			CAG ATC AGCTTCTCT		
			GTC TAG TTGAAGAGA		
			C_ _ A		
GAM23	SMARCA3	3'	AGAGAAGCTTCATGTTTG 246	TCATC	
			CAGAC AAGCTTCTCT		
			GTTTG TTCGAAGAGA		
			TAC_		
GAM23	SMARCA3	3'	AGAGAAGCTTCATGTTTG 66	TCATC	
			CAGAC AAGCTTCTCT		
			GTTTG TTCGAAGAGA		
			TAC_		
GAM23	SMG1	3'	AGACAGTAGATGAGTCTG 138	AA _	
			CAGACTCATC GCT TCT		
			GTCTGAGTAG TGA AGA		
			A_ C		
GAM23	SNCAIP	5'	AGAAAGGGGGTGAGTCTG 399	AAG C	
			CAGACTCATC CTT TCT		
			GTCTGAGTGG GAA AGA		
			GG_ _		
GAM23	SYNGR1	3'	AGGGGAGCGATGAGCTG 86	A AA	
			CAG CTCATC GCTTCTCT		
			GTC GAGTAG CGAGGGGA		
			- -		
GAM23	UCP2	5'	AGAGAAGCTTGATCTTGAG 68	_____	
			CTC ATCAAGCTTCTCT		
			GAG TAGTTCGAAGAGA		
			GTTC		
GAM23	BMF	3'	AGAGGCTGATGTGTCTG 229	T A	
			CAGAC CATCA GCTTCT		
			GTCTG GTAGT CGGAGA		
			T _		
GAM23	BNIP2	3'	AGAGAATGTGATGAGTT 278	AGC	
			GACTCATCA TTCTCT		

			TTGAGTAGT AAGAGA		
			GT_		
GAM23	DDX33	3'	AGAGAAGCCTTGGAATC 171	C AT _	
			GA TC CAAG CTTCTCT		
			CT AG GTTC GAAGAGA		
			A _ C		
GAM23	EML4	3'	AGAAACTTTGGATGAGTT 168	_ C	
			GACTCATC AAG TTCT		
			TTGAGTAG TTC AAGA		
			GT A		
GAM23	EPB41L4	3'	AGAGAAGAAATGGGTCT 187	CAAG	
			AGACTCAT CTTCTCT		
			TCTGGGTA GAAGAGA		
			AA_		
GAM23	FLJ11588	5'	AGAGAAGCAGAACGGCCTG 199	A CA AA	
			CAG CT TC GCTTCTCT		
			GTC GG AG CGAAGAGA		
			C CA A_		
GAM23	FLJ20150	3'	AGAGAAGCCTGTGGCT 153	A T T A	
			AG C CA CA GCTTCTCT		
			TC G GT GT CGAAGAGA		
			_ _ _ C		
GAM23	FLJ20507	3'	AGATGTTGATGAGGCTG 154	A G T	
			CAG CTCATCAA C TCT		
			GTC GAGTAGTT G AGA		
			G _ T		
GAM23	FLJ20507	3'	AGATGTTGATGAGGCTG 261	A G T	
			CAG CTCATCAA C TCT		
			GTC GAGTAGTT G AGA		
			G _ T		
GAM23	FLJ20972	3'	AGAGAAGCAGTTGGCATCTG 205	C_ TCAA	
			CAGA TCA GCTTCTCT		
			GTCT GGT CGAAGAGA		
			AC TGA_		
GAM23	FLJ22233	3'	AGAGAAGCTAGAAGTC 204	CA A	
			GACT TC AGCTTCTCT		
			CTGA AG TCGAAGAGA		
			_ A		
GAM23	FLJ23191	3'	AGAGAAGTTGTGACCTG 198	AC CA	
			CAG TCAT AGCTTCTCT		

GTC AGTG TTGAAGAGA
 C_ _
 GAM23 FLJ23468 5' AGAGAAACCAGCTGAGTCTG 200 TCAA ____
 CAGACTCA GCT TCTCT
 ||||| || |||||
 GTCTGAGT CGA AGAGA
 ____ CCAA
 GAM23 GIT2 3' AGAGAAGCATCAGTCT 133 C CAA
 AGACT AT GCTTCTCT
 ||||| || |||||
 TCTGA TA CGAAGAGA
 C ____
 GAM23 GIT2 3' AGAGAAGCATCAGTCT 231 C CAA
 AGACT AT GCTTCTCT
 ||||| || |||||
 TCTGA TA CGAAGAGA
 C ____
 GAM23 GIT2 3' AGAGAAGCATCAGTCT 232 C CAA
 AGACT AT GCTTCTCT
 ||||| || |||||
 TCTGA TA CGAAGAGA
 C ____
 GAM23 GRID1 3' AGAGAAGCCTAGGTGGGCT 285 A AA_
 AG CTCATC GCTTCTCT
 || ||||| |||||
 TC GGGTGG CGAAGAGA
 _ ATC
 GAM23 GT650 3' AAGCTTTCTATGAGTTTG 230 C_
 CAGACTCAT AAGCTT
 ||||| |||||
 GTTTGAGTA TTCGAA
 TCT
 GAM23 IKKE 3' AGGACTGTGAGTCTG 124 CA C
 CAGACTCAT AG TTCT
 ||||| || |||||
 GTCTGAGTG TC AGGA
 _ _
 GAM23 KIAA0254 5' AGAGGACCGCGATGAGTC 131 AA ____
 GACTCATC GC TTCTCT
 ||||| || |||||
 CTGAGTAG CG AGGAGA
 _ CC
 GAM23 KIAA1026 3' AGAGAAGCTGCCTCAGTCTG 292 CATCA
 CAGACT AGCTTCTCT
 ||||| |||||
 GTCTGA TCGAAGAGA
 CTCCG
 GAM23 KIAA1163 3' AGAGAAGCATGTCTGAGTT 331 T_ A
 GACTCA CA GCTTCTCT
 ||||| || |||||

			TTGAGT GT CGAAGAGA		
			CT A		
GAM23	KIAA1598	3'	AGAAGCTTCTGTTTTGGGTCTG 161	TC_____	
			CAGACTCA AAGCTTCT		
			GTCTGGGT TTCGAAGA		
			TTTGTC		
GAM23	KIAA1853	3'	AGAAGCAATGGGTCTG 287	CAA	
			CAGACTCAT GCTTCT		
			GTCTGGGTA CGAAGA		
			A__		
GAM23	LOXL4	3'	AGAGAAGCTGGTGGATC 213	CT A	
			GA CATCA GCTTCTCT		
			CT GTGGT CGAAGAGA		
			AG _		
GAM23	METAP1	3'	AGAGAAGCGTGAAGTTTG 298	CA A	
			CAGACT TCA GCTTCTCT		
			GTTTGA AGT CGAAGAGA		
			_ G		
GAM23	MGC11034	3'	AGAGAAGCTCTTTGAAGTT 211	_ TCA	
			GA CT CA AGCTTCTCT		
			TTGA GT TCGAAGAGA		
			A TTC		
GAM23	MGC14128	3'	AGAAGCTTTGAGAGCCTG 222	A A _	
			CAG CTC TCAA GCTTCT		
			GTC GAG AGTT CGAAGA		
			C _ T		
GAM23	MGC16175	5'	AGAGGCTGTGAGTCTG 219	CA	
			CAGACTCAT AGCTTCT		
			GTCTGAGTG TCGGAGA		
			—		
GAM23	MGC2752	5'	AGAGAAGCTCAGTAGAATC 327	C _ CA	
			GA TC AT AGCTTCTCT		
			CT AG TG TCGAAGAGA		
			A A AC		
GAM23	MGC34923	3'	AGAGAAGTAGGAAGAGCCTG 254	A A AA	
			CAG CTC TC GCTTCTCT		
			GTC GAG AG TGAAGAGA		
			C A GA		
GAM23	NR1I3	5'	AGAGAAGCAGGAGTCTG 89	ATCAA	
			CAGACTC GCTTCTCT		

			GTCTGAG CGAAGAGA		
			GA__		
GAM23	NYD-SP15	3'	AGAGAAGAAATATTTGAGTCTG 208	TCAAG__	
			CAGACTCA CTTCTCT		
			GTCTGAGT GAAGAGA		
			TTATAAA		
GAM23	OSBPL8	5'	AGAGAAGTTGGGGTCTG 177	ATCAA	
			CAGACTC GCTTCTCT		
			GTCTGGG TGAAGAGA		
			GT__		
GAM23	PLEKHA4	5'	AGAGACCCTGTGAGTCTG 178	CA CT	
			CAGACTCAT AG TCTCT		
			GTCTGAGTG TC AGAGA		
			__ CC		
GAM23	PRKWNK2	3'	AGAGATGATTGAGTCTG 372	_ AGCT	
			CAGACTCA TCA TCTCT		
			GTCTGAGT AGT AGAGA		
			T ____		
GAM23	PSMD4	3'	AGGGTAGCTGAGTCTG 63	TCAA T	
			CAGACTCA GCT CTCT		
			GTCTGAGT CGA GGGA		
			____ T		
GAM23	RIS1	3'	AGAGAAGCTCTTTGTATCTG 337	CT TCA	
			CAGA CA AGCTTCTCT		
			GTCT GT TCGAAGAGA		
			AT TTC		
GAM23	RNF24	3'	AGAGGAGTGGATGAGCCTG 114	A AA	
			CAG CTCATC GCTTCTCT		
			GTC GAGTAG TGAGGAGA		
			C G_		
GAM23	SNURF	3'	AGAAAAGCGGGTTTTGGGTCTG 96	TCAA__ C	
			CAGACTCA GCTT TCT		
			GTCTGGGT CGAA AGA		
			TTTGGG A		
GAM23	SULT4A1	3'	AGAGAAGCTTGTGTTTTTG 284	CT T	
			CAGA CA CAAGCTTCTCT		
			GTTT GT GTTCGAAGAGA		
			TT _		
GAM23	SV2B	3'	AGAGAATTGTGTGAGTCTG 135	_ GC	
			CAGACTCAT CAA TTCTCT		

			GTCTGAGTG GTT AAGAGA		
			T _		
GAM23	SZF1	5'	AGAGAAGCCTAGATATCTG 147	CTC AA_	
			CAGA ATC GCTTCTCT		
			GTCT TAG CGAAGAGA		
			A_ ATC		
GAM23	TLR10	5'	AGAGAGGGTATTGAGTCTG 210	TCAAG	
			CAGACTCA CTTCTCT		
			GTCTGAGT GGAGAGA		
			TATG_		
GAM23	ZNF185	3'	AGAGGAGCTTGTGAATC 111	C T	
			GA TCA CAAGCTTCTCT		
			CT AGT GTTCGAGGAGA		
			A _		
GAM23	LOC113612	3'	AGAAGGATGAGTTTG 300	AAG	
			CAGACTCATC CTTCT		
			GTTTGAGTAG GAAGA		
			—		
GAM23	LOC133539	3'	AGAGAAGCCCAGGATGGTC 312	T AA_	
			GAC CATC GCTTCTCT		
			CTG GTAG CGAAGAGA		
			_ GACC		
GAM23	LOC139221	5'	AGAGAAGCACATGACCTG 313	AC CAA	
			CAG TCAT GCTTCTCT		
			GTC AGTA CGAAGAGA		
			C_ CA_		
GAM23	LOC142941	3'	AAGTTTATTGTAATGAGTCTG 345	— —	
			CAGACTCAT CAA GCTT		
			GTCTGAGTA GTT TGAA		
			AT ATT		
GAM23	LOC145717	5'	AGAGAGTGGGGGTGAGTCTG 279	AA_ T	
			CAGACTCATC GCT CTCT		
			GTCTGAGTGG TGA GAGA		
			GGG _		
GAM23	LOC147229	3'	AGAGAAGCTGGCAAGAGCTG 325	A ATCA_	
			CAG CTC AGCTTCTCT		
			GTC GAG TCGAAGAGA		
			_ AACGG		
GAM23	LOC147658	3'	AGAAAAGTTTGAAGTC 326	CA C	
			GACT TCAAGCTT TCT		

		CTGA AGTTTGAA AGA		
		— A		
GAM23	LOC147920 3'	AGAGAAGCCTGAGGAATTT 328	C A A	
		AGA TC TCA GCTTCTCT		
		TTT AG AGT CGAAGAGA		
		A G C		
GAM23	LOC148894 5'	AGAGAAGCTCCGTGGGCCTG 347	A CA	
		CAG CTCAT AGCTTCTCT		
		GTC GGGTG TCGAAGAGA		
		C CC		
GAM23	LOC150606 3'	AGAGAAGCTGGGTGATCTG 349	C A	
		CAGA TCATC AGCTTCTCT		
		GTCT AGTGG TCGAAGAGA		
		— G		
GAM23	LOC150606 3'	AGAGAAGCTTGTGGTC 350	T T	
		GAC CA CAAGCTTCTCT		
		CTG GT GTTCGAAGAGA		
		— —		
GAM23	LOC152220 3'	AGAGTATTTCTTGATGAATTT 351	C CTT__	
		AGA TCATCAAG CTCT		
		TTT AGTAGTTC GAGA		
		A TTTAT		
GAM23	LOC155382 3'	AGAGAAGCTGCAGGAGCTG 356	A ATCA	
		CAG CTC AGCTTCTCT		
		GTC GAG TCGAAGAGA		
		— GACG		
GAM23	LOC157621 3'	AGAGGGCGAAATGAGTCT 358	CAA T	
		AGACTCAT GCT CTCT		
		TCTGAGTA CGG GAGA		
		AAG _		
GAM23	LOC161528 5'	AGAGAGTGGGGGTGAGTCTG 342	AA_ T	
		CAGACTCATC GCT CTCT		
		GTCTGAGTGG TGA GAGA		
		GGG _		
GAM23	LOC197114 5'	AGAGAAGCCCGAGGGGGCTG 369	A A AA	
		CAG CTC TC GCTTCTCT		
		GTC GGG AG CGAAGAGA		
		G G CC		
GAM23	LOC199883 3'	AGAAAGGCGGTGAGTC 370	AA C	
		GACTCATC GCTT TCT		

		CTGAGTGG CGGA AGA	
		— A	
GAM23	LOC200020 3'	AGAAAAGGCGGTGAGTC 371	AA C
		GACTCATC GCTT TCT	
		CTGAGTGG CGGA AGA	
		— A	
GAM23	LOC200226 3'	AGAGAAGCTCGTGAATGTT 365	— CA
		GAC TCAT AGCTTCTCT	
		TTG AGTG TCGAAGAGA	
		TA C_	
GAM23	LOC204820 5'	AGAGAAGCCAGGCCAGCTG 373	A CA AA
		CAG CT TC GCTTCTCT	
		GTC GA GG CGAAGAGA	
		_ CC AC	
GAM23	LOC219392 5'	AGAGAAATCCTAGATGAGTC 377	A C_
		GACTCATC AG TTCTCT	
		CTGAGTAG TC AAGAGA	
		A CTA	
GAM23	LOC219800 3'	AGAGAAGCTTGGGAGCCT 389	A A
		AG CTC TCAAGCTTCTCT	
		TC GAG GGTTCGAAGAGA	
		C _	
GAM23	LOC220753 5'	AGAGAAGCCAGAGGTGTG 388	G CA AA
		CA ACT TC GCTTCTCT	
		GT TGG AG CGAAGAGA	
		G _ AC	
GAM23	LOC220776 3'	AGAGGGGTGATGATAAACTG 283	AC_ AA
		CAG TCATC GCTTCTCT	
		GTC AGTAG TGGGGAGA	
		AAAT _	
GAM23	LOC221454 5'	AGAGAAGATGAAAGTTTG 382	CA AG
		CAGACT TCA CTTCTCT	
		GTTTGA AGT GAAGAGA	
		A_ A_	
GAM23	LOC222444 3'	AGAGAAGCCCAGGATGGTC 392	T AA_
		GAC CATC GCTTCTCT	
		CTG GTAG CGAAGAGA	
		_ GACC	
GAM23	LOC222962 3'	AGAGGGGAGGTAAGTCTG 387	C AAG
		CAGACT ATC CTTCTCT	

			GTCTGA TGG GGGGAGA		
			A A__		
GAM23	LOC245727	5'	AGAGAGTGGGGGTGAGTCTG 376	AA_ T	
			CAGACTCATC GCT CTCT		
			GTCTGAGTGG TGA GAGA		
			GGG _		
GAM23	LOC253525	5'	AGAGAAGCTGCAGGTTTG 401	CATCA	
			CAGACT AGCTTCTCT		
			GTTTGG TCGAAGAGA		
			ACG__		
GAM23	LOC254249	5'	AGAGAAGTTTGTAATTTG 397	CTCAT	
			CAGA CAAGCTTCTCT		
			GTTT GTTTGAAGAGA		
			AAAT_		
GAM23	LOC255475	5'	AGAGAAGCCGAGCTCTG 403	_ ATCAA	
			CAGA CTC GCTTCTCT		
			GTCT GAG CGAAGAGA		
			C C__		
GAM23	LOC51026	3'	AGAACCCTTGATGAGACT 146	A C_	
			AG CTCATCAAG TTCT		
			TC GAGTAGTTC AAGA		
			A CC		
GAM23	LOC91308	5'	AGAAGAGATGAGTTTG 274	AAG	
			CAGACTCATC CTTCT		
			GTTTGAGTAG GAAGA		
			A__		
GAM24	CASP10	3'	ATACAACCTGATGTCATATTCC 223	C ____ C_ A	
			ATTTTGGA TG GA AC CAG TTGTA T		
			AC CT TG GTC AACAT A		
			_ TATAC TA C		
GAM24	CASP10	3'	ATACAACCTGATGTCATATTCC 224	C ____ C_ A	
			ATTTTGGA TG GA AC CAG TTGTA T		
			AC CT TG GTC AACAT A		
			_ TATAC TA C		
GAM24	CHRNA3	5'	TTGGGTCCACTTCGGA 49	A A C	
			TCC AA TG GAACCCAG		
			AGG TT AC CTTGGGTT		
			C C _		
GAM24	LANCL1	3'	TACAATCTGGACTTGGTA 100	G C_	
			TGC AA CCAGATTGTA		

			ATG TT GGTCTAACAT		
			G CA		
GAM24	MS4A3	3'	ACATCTGGGTTCAAATTCTG 101	A GC	T
			CA AAT GAACCCAGAT GT		
			GT TTA CTTGGGTCTA CA		
			C AA _		
GAM24	SLC1A4	3'	TACAATTGTCCCAGTTCGCAT 64	CCA__	
			ATGCGAAC GATTGTA		
			TACGCTTG TTAACAT		
			ACCCTG		
GAM24	ALLC	5'	TACAAGGATTTCGCATTCTGGG 162	A C_ AGA	
			TCCA AATGCGAA CC TTGTA		
			GGGT TTACGCTT GG AACAT		
			C TA _		
GAM24	APOL6	3'	CTGGGTTCACATTTTGGA 206	C	
			TCCAAAATG GAACCCAG		
			AGGTTTTAC CTTGGGTC		
			A		
GAM24	CBX6	3'	TTGGGCTCCATTCTGGA 128	A C A	
			TCCA AATG GA CCCAG		
			AGGT TTAC CT GGGTT		
			C _ C		
GAM24	FLJ10055	3'	TTGGGAGTCCCATTTTGGA 156	C A_	
			TCCAAAATG GA CCCAG		
			AGGTTTTAC CT GGGTT		
			C GA		
GAM24	FLJ22059	5'	CAGTCTGGACCAGCACCTTGGA 191	AA GAAC	
			TCCAA TGC CCAGATTG		
			AGGTT ACG GGTCTGAC		
			CC ACCA		
GAM24	KCNH8	3'	TTGGGTTCACATTCTGGA 252	A C	
			TCCA AATG GAACCCAG		
			AGGT TTAC CTTGGGTT		
			C A		
GAM24	KIAA0870	3'	TTGGGTCTGCATTTTGGA 339	A	
			TCCAAAATGCG ACCCAG		
			AGGTTTTACGT TGGGTT		
			C		
GAM24	KIAA1157	3'	ACAGTATTCCATTTTGGA 296	C CCCAG	
			TCCAAAATG GAA ATTGT		

			AGGTTTTAC CTT	TGACA	
			— A —		
GAM24	PRO1048	3'	ACAATGAGTTTGCATTTT	163	C GA
			AAAATGCGAAC CA TTGT		
			TTTTACGTTTG GT AACA		
			A —		
GAM24	PRO1787	3'	ACAATTCGCGCATTTTG	165	AACCCA
			CAAAATGCG GATTGT		
			GTTTTACGC TTAACA		
			C —		
GAM24	UBE2G1	3'	TACAGATGATTACGCATTTTG	67	AACC GA
			CAAAATGCG CA TTGTA		
			GTTTTACGC GT GACAT		
			ATTA A_		
GAM24	LOC122402	3'	TACTTCTTGTTTCACATTTTGG	306	C C TT
	A		TCCAAAATG GAACC AGA GTA		
			AGGTTTTAC CTTGG TCT CAT		
			A T T_		
GAM24	LOC153592	3'	GGAATTCAGCATTTTGGA	355	_ C_
			TCCAAAATGC GAA CC		
			AGGTTTTACG CTT GG		
			A AA		
GAM24	LOC256158	5'	ACAATCTGAACGTCTGGG	404	AAAT AACC
			TCCA GCG CAGATTGT		
			GGGT TGC GTCTAACA		
			C_ AA_		
GAM25	ITGA5	3'	CTCAGATCCAGGGACAGAGG	264	GTTAGA A_
			TCTCTG CC GATCTGAG		
			GGAGAC GG CTAGACTC		
			AG_ AC		
GAM25	SF3B3	3'	GCTCTAGAATCTAACCAGA	116	CCAGA _
			TCTGGTTAGA TCT GAGC		
			AGACCAATCT AGA CTCG		
			A_ T		
GAM25	SLC4A4	3'	GCTCAGAGTTGTTAACCAGA	71	AC A
			TCTGGTTAG CAG TCTGAGC		
			AGACCAATT GTT AGACTCG		
			_ G		
GAM25	ZNF180	3'	CTCAGACCTGAATCAGAGA	120	AGAC A
			TCTCTGGTT CAG TCTGAG		

			AGAGACTAA	GTC AGACTC		
			_____ C			
GAM25	AP1G2	5'	GCCCAGGCACGCCCGACCAGAG	233	AGACCAGA	A
	A		TCTCTGGTT	TCTG GC		
			AGAGACCAG	GGAC CG		
			CCCGCAC_	C		
GAM25	BCL2L1	3'	GCCCAGATCTGGTCCCTTGCAG	241	GTTA_	A
			CTG	GACCAGATCTG GC		
			GAC	CTGGTCTAGAC CG		
			GTTCC	C		
GAM25	FLJ25012	5'	CTCAGATCTGAAAAGCACAAGA	250	C _	AGAC
			TCT TG GTT	CAGATCTGAG		
			AGA AC CGA	GTCTAGACTC		
			_ A AAA_			
GAM25	FLJ31952	3'	CAAATCTGGTTCTGAAAG	253	GG _	C
			CT	TTAGA CCAGAT TG		
			GA	AGTCT GGTCTA AC		
			A_	T A		
GAM25	MDS025	3'	CTCAGACCTGGTTTGAGATAGA	184	G_	A
			TCTG	TTAGACCAG TCTGAG		
			AGAT	AGTTTGGTC AGACTC		
			AG	C		
GAM25	MGC32043	3'	GCTCAGATCTGATGCTTCAAGA	249	GGTT AC_	
			TCT	AG CAGATCTGAGC		
			AGA	TC GTCTAGACTCG		
			ACT_	GTA		
GAM25	MSI2	3'	CTCCCCATCCCAACCAGAGA	245	AGACCA	CT_
			TCTCTGGTT	GAT GAG		
			AGAGACCAA	CTA CTC		
			CC_	CCC		
GAM25	ZNF271	5'	GCTCAGATCTGGTTAAACATCA	395	_	A
	GAGA		TCTCTG	GTT GACCAGATCTGAGC		
			AGAGAC	CAA TTGGTCTAGACTCG		
			TA	A		
GAM25	LOC144508	5'	GCTCAGATCCATGTGCCAGGGA	362	TAGACCA	
			TCTCTGGT	GATCTGAGC		
			AGGGACCG	CTAGACTCG		
			TGTAC_			
GAM25	LOC145845	3'	CTCAAATCCCACCAGAGA	346	TAGACCA	C
			TCTCTGGT	GAT TGAG		

			AGAGACCA	CTA ACTC	
			CC_____	A	
GAM26	CDH19	3'	GAAAATTTAAAGGAGCAA	182	A_
			TTGC CTTTAAATTTTC		
			AACG GAAATTTAAAAG		
			AG		
GAM26	CRYGS	5'	TGGGAAAACCAAGTCTATGCACC	152	T CTTTAAA_
	AA		TTGGT GCA	TTTTCCCA	
			AACCA CGT	AAAAGGGT	
			_ ATCTGACC		
GAM26	CYP1B1	3'	GAAAATTGAAAAGTACAATAA	33	C A_
			TTGGTTG ACTTT AATTTTC		
			AATCAAC TGAAA TTAAAAG		
			A AG		
GAM26	GLI3	3'	GGAAAAAAGACTGCAACCAA	35	C AAA
			TTGGTTGCA TTT TTTTCC		
			AACCAACGT AGA AAAAGG		
			C AA_		
GAM26	PCLO	3'	GAAGATAATGCAACCAA	391	CTTTAA
			TTGGTTGCA	ATTTTC	
			AACCAACGT	TAGAAG	
			AA_____		
GAM26	PPP2R5A	3'	TGGGAAAGTAAACCAA	102	GC TAAATT
			TTGGTT ACTT	TCCCA	
			AACCAA TGAA	AGGGT	
			A_ _____		
GAM26	PTER	3'	TGAGAAAATTTAAAGTGTTTCT	207	TT C
	AG		TTGG GCACTTTAAATTTTC	CA	
			GATC TGTGAAATTTAAAAG	GT	
			TT	A	
GAM26	RFX5	3'	GGGAAAAGCAGTAAACCAA	39	GC TTAAA
			TTGGTT ACT	TTTTCCC	
			AACCAA TGA	AAAAGGG	
			A_ CG_____		
GAM26	CSMD1	3'	GGAGTATTAAAGTGGAACCAA	301	G ATT
			TTGGTT CACTTTAA	TTCC	
			AACCAA GTGAAATT	GAGG	
			G	AT_	
GAM26	MGC15438	3'	GAAAGAAAGCGCAGCCAA	220	A AAA
			TTGGTTGC CTTT	TTTTC	

			AACCGACG GAAA GAAAG		
			C ____		
GAM26	NYD-SP18	3'	GGAGAAAACCTGCAACCAA 217	C	AAAT
			TTGGTTGCA TTT TTTCC		
			AACCAACGT AAA AGAGG		
			C ____		
GAM26	OLFM3	3'	GGAAAAATAATGTAACCAA 340	C	TAAA
			TTGGTTGCA TT TTTTCC		
			AACCAATGT AA AAAAGG		
			_ TA__		
GAM26	RPL13A	3'	GGGAAGATGCACAACCAA 115	CACTTTAA	
			TTGGTTG ATTTTCCC		
			AACCAAC TAGAAGGG		
			ACG_____		
GAM26	LOC129452	3'	AGAATGGACAAGCGCAACCAA 310	A	TAA_
			TTGGTTGC CTT ATTTT		
			AACCAACG GAA TAAGA		
			C CAGG		
GAM26	LOC150197	3'	GGATTAAAGTGGAACCAA 335	G	ATTT
			TTGGTT CACTTTAA TCC		
			AACCAA GTGAAATT AGG		
			G ____		
GAM26	LOC162239	3'	GGAAATTATAAATGGCAACCAA 344	AC	AAT
			TTGGTTGC TTTA TTTCC		
			AACCAACG AAAT AAAGG		
			GT ATT		
GAM26	LOC219972	3'	GAAATGGCAAGTGCAACCAA 379	TAA	
			TTGGTTGCACTT ATTTT		
			AACCAACGTGAA TAAAG		
			CGG		
GAM27	DDX6	3'	ATTGTGACAAGAATTGTTACC 80	C	CCC C
			GG AACGA CT GTCACAAT		
			CC TTGTT GA CAGTGTTA		
			A AA_ A		
GAM27	LOC126917	3'	GCAGTGGGTCTGTTGCCA 309	_ _	C
			TGGCAAC GACCC CT GT		
			ACCGTTG CTGGG GA CG		
			T T _		
GAM27	LOC170395	3'	TATTGTTTCTGGGTGTTGCCA 316	G	CTCGTC
			TGGCAAC ACCC ACAATA		

			ACCGTTG TGGG TGTTAT	
			_ TCTT_	
GAM28	ABCC3	3'	TGCCCCTGGCTGTGCTCTAC 170	C A T
			GTG AG ACA CCAGGGGCA	
			CAT TC TGT GGTCCCCGT	
			C G C	
GAM28	CASP3	3'	TGCCCCTGGATCTACCAGCAT 225	AGAAC_
			GTGC ATCCAGGGGCA	
			TACG TAGGTCCCCGT	
			ACCATC	
GAM28	CASP3	3'	TGCCCCTGGATCTACCAGCAT 79	AGAAC_
			GTGC ATCCAGGGGCA	
			TACG TAGGTCCCCGT	
			ACCATC	
GAM28	EMS1	3'	CCCTGGATCCTCACACTA 90	CA AC
			TAGTG GA ATCCAGGG	
			ATCAC CT TAGGTCCC	
			A_ CC	
GAM28	EMS1	3'	CCCTGGATCCTCACACTA 240	CA AC
			TAGTG GA ATCCAGGG	
			ATCAC CT TAGGTCCC	
			A_ CC	
GAM28	MLLT2	3'	TGCCCCTGGACATGTTTCCTAC 97	CA _
			GTG GAACA TCCAGGGGCA	
			CAT TTTGT AGGTCCCCGT	
			CC AC	
GAM28	TACC1	3'	TGCCCCCAGATGTTTCCTGGGCT 104	G _ CA
	G		TAGT CAG AACATC GGGGCA	
			GTCG GTC TTGTAG CCCCCT	
			G C AC	
GAM28	TNFSF6	3'	CCAGGTGTTCTACACTCA 42	T C CA
			A AGTG AGAACATC GG	
			A TCAC TCTTGTGG CC	
			C A A_	
GAM28	UBB	3'	TGGCATTACTCTGCACTATA 166	AC_ _
			TATAGTGCAGA AT CCA	
			ATATCACGTCT TA GGT	
			CAT C	
GAM28	AKAP10	3'	TGCCCCTTTGGAATTCTGCACT 113	CA _
			AGTGCAGAA TCCA GGGGCA	

			TCACGTCTT AGGT CCCCCT		
			A_ TT		
GAM28	DECR2	3'	GCCCCTCTGTCTCTGCAC 176	_ TCC	
			GTGCAGA ACA AGGGGC		
			CACGTCT TGT TCCCCG		
			C C_		
GAM28	KIAA0240	3'	GCCCCTGTGTCCCACTA 383	CA A TC	
			TAGTG GA CA CAGGGGC		
			ATCAC CT GT GTCCCCG		
			C_ _ _		
GAM28	MGC16385	5'	GCCCCTGGACGTTTCTGCCGC 255	_ _ A	
			GTG CAGAA C TCCAGGGGC		
			CGC GTCTT G AGGTCCCCG		
			C T C		
GAM28	MGC5139	5'	GCCCCTGGGCACACTGTA 305	CAGAACA	
			TATAGTG TCCAGGGGC		
			ATGTCAC GGGTCCCCG		
			AC_		
GAM28	P5-1	3'	CCCCTGGATGCCCTAACCCT 110	C_ AA_	
			AGTG AG CATCCAGGGG		
			TCAC TC GTAGGTCCCC		
			CAA CCC		
GAM28	TED	3'	CCCCTGGGCCCTGCCTA 143	T AACA	
			TAG GCAG TCCAGGGG		
			ATC CGTC GGGTCCCC		
			_ CC_		
GAM28	LOC133418	3'	TGCTCTAAAGCTCTGCACTA 311	ACATCCA	
			TAGTGCAGA GGGGCA		
			ATCACGTCT TCTCGT		
			CGAAA_		
GAM28	LOC152402	3'	GCCCTTACATTCTGCACT 353	CATCC	
			AGTGCAGAA AGGGGC		
			TCACGTCTT TTCCCG		
			ACA_		
GAM28	LOC158677	3'	TGCCCCTGGATATCAGCAATAT 360	G A AC	
	A		TATA TGC GA ATCCAGGGGCA		
			ATAT ACG CT TAGGTCCCCGT		
			A A A_		
GAM28	LOC221715	3'	CCACTGTGCTTGCACTA 390	AA TC _	
			TAGTGCAG CA CAG GG		

			ATCACGTT GT GTC CC		
			C_ _ A		
GAM28	LOC254746	3'	TGGCATTACTCTGCACTATA 394	AC_ _	
			TATAGTGCAGA AT CCA		
			ATATCACGTCT TA GGT		
			CAT C		
GAM28	LOC255098	3'	TGCTCTAAAGCTCTGCACTA 396	ACATCCA	
			TAGTGCAGA GGGGCA		
			ATCACGTCT TCTCGT		
			CGAAA_		
GAM29	ADAM19	3'	CTGATGGAGATGCTCAAGGC 228	AG	TATGG
			GCCTT GCATCTCC CAG		
			CGGAA CGTAGAGG GTC		
			CT TA_		
GAM29	LFG	3'	TGCCACAGGCCTAAGGCT 319	ATCTC	A
			AGCCTTAGGC CT TGGCA		
			TCGGAATCCG GA ACCGT		
			_ C		
GAM29	NOLA2	5'	GGAAGTGATGCCTAAAGCT 393	C	_
			AGC TTAGGCATC TCC		
			TCG AATCCGTAG AGG		
			A TGA		
GAM29	FLJ10751	3'	CCAGAGACACCTGAGGC 158	CA	CTA
			GCCTTAGG TCTC TGG		
			CGGAGTCC AGAG ACC		
			AC _		
GAM29	FLJ10751	3'	CCAGAGACACCTGAGGC 159	CA	CTA
			GCCTTAGG TCTC TGG		
			CGGAGTCC AGAG ACC		
			AC _		
GAM29	FLJ10925	5'	CTGCCCCCAGGGACACCTAAGG 160	CA T	AT_
		C	GCCTTAGG TC CCT GGCAG		
			CGGAATCC AG GGA CCGTC		
			AC _ CCC		
GAM29	KIAA1118	3'	GTGGTTGAGATGCCCCACGGCT 289	TTA	CT G
			AGCC GGCATCTC AT GC		
			TCGG CCGTAGAG TG TG		
			CAC T_ G		
GAM29	KIAA1649	3'	CTGCCATTTCTGTGCCTAGGCT 215	T	CTCCT
			AGCCT AGGCAT ATGGCAG		

			TCGGA TCCGTG TACCGTC		
			— TCTT—		
GAM29	LIMR	3'	CTGCCATCTGCTGCCTAGGC 157	T	TCTCCT
			GCCT AGGCA ATGGCAG		
			CGGA TCCGT TACCGTC		
			— CGTC—		
GAM29	MGC14161	5'	CCAGAGAGATGCCAAAGGC 221	A	CTA
			GCCTT GGCATCTC TGG		
			CGGAA CCGTAGAG ACC		
			A AG—		
GAM29	NJMU-R1	3'	CATGAAGAAATGCCTGAAGC 188	C	C C—
			GC TTAGGCAT TC TATG		
			CG AGTCCGTA AG GTAC		
			A A AA		
GAM29	SEMA3E	3'	CTGTTGTGAGAAATGCCCAGGC 119	TA	C C TG
	T		AGCCT GGCAT TC TA GCAG		
			TCGGA CCGTA AG GT TGTC		
			C— A A GT		
GAM29	YKT6	3'	CTGCCATAGATACCCTAAG 106	CATCTC	
			CTTAGG CTATGGCAG		
			GAATCC GATACCGTC		
			CATA—		
GAM29	LOC142972	5'	GCCACAGGAGATGCCCAAAGC 271	C A	A
			GC TT GGCATCTCCT TGGC		
			CG AA CCGTAGAGGA ACCG		
			A C C		
GAM29	LOC143689	3'	TGCCATAAGCTCAAGGCT 318	AG ATCTCC	
			AGCCTT GC TATGGCA		
			TCGGAA CG ATACCGT		
			CT A—		
GAM29	LOC148930	5'	CCATAGGGAGCCTAAG 332	A T	
			CTTAGGC TC CCTATGG		
			GAATCCG AG GGATACC		
			— —		
GAM29	LOC220469	3'	CCAAGGGATGCCCAAAGC 317	C A	T A
			GC TT GGCATC CCT TGG		
			CG AA CCGTAG GGA ACC		
			A C — —		
GAM29	LOC253782	3'	CATAAGAGCACCTAAGGC 398	CAT	C
			GCCTTAGG CTC TATG		

CGGAATCC GAG ATAC

AC_ A

GAM29 LOC92078 5' TGCCCAGAGGCCTAAGGCT 282 A CCTAT

AGCCTTAGGC TCT GGCA

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TCGGAATCCG AGA CCGT

G C_____